



1/24

SEQUENCE LISTING

<110> Berlin, Vivian
Chiu, Maria Isabel
Cottarel, Guillaume
Damagnez, Veronique

<120> IMMUNOSUPPRESSANT TARGET PROTEINS

<130> APBI-P06-036

<140> US 09/517,491

<141> 2000-03-02

<150> US 08/360,144

<151> 1994-12-20

<150> US 08/250,795

<151> 1994-05-27

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 486

<212> DNA

<213> Mouse

<220>

<221> CDS

<222> (1)...(486)

<400> 1

ctc	acc	cgt	cac	aat	gca	gcc	aac	aag	atc	ttg	aag	aac	atg	tgt	gaa	48
Leu	Thr	Arg	His	Asn	Ala	Ala	Asn	Lys	Ile	Leu	Lys	Asn	Met	Cys	Glu	
1				5				10					15			

cac	agc	aac	acg	ctg	gtc	cag	cag	gcc	atg	atg	gtg	agt	gaa	gag	ctg	96
His	Ser	Asn	Thr	Leu	Val	Gln	Gln	Ala	Met	Met	Val	Ser	Glu	Glu	Leu	
			20					25					30			

att	cgg	gta	gcc	atc	ctc	tgg	cat	gag	atg	tgg	cat	gaa	ggc	ctg	gaa	144
Ile	Arg	Val	Ala	Ile	Leu	Trp	His	Glu	Met	Trp	His	Glu	Gly	Leu	Glu	
		35				40					45					

gag	gca	tct	cgc	ttg	tac	ttt	ggg	gag	agg	aac	gtg	aaa	ggc	atg	ttt	192
Glu	Ala	Ser	Arg	Leu	Tyr	Phe	Gly	Glu	Arg	Asn	Val	Lys	Gly	Met	Phe	
	50					55				60						

gag	gtg	ctg	gag	ccc	ctg	cat	gct	atg	atg	gaa	cgg	ggg	ccc	cgg	act	240
Glu	Val	Leu	Glu	Pro	Leu	His	Ala	Met	Met	Glu	Arg	Gly	Pro	Arg	Thr	
	65				70					75					80	

ctg	aag	gaa	aca	tcc	ttt	aat	cag	gca	tat	ggc	cga	gat	tta	atg	gag	288
Leu	Lys	Glu	Thr	Ser	Phe	Asn	Gln	Ala	Tyr	Gly	Arg	Asp	Leu	Met	Glu	
				85					90						95	

gca	caa	gaa	tgg	tgt	cga	aag	tac	atg	aag	tcg	ggg	aac	gtc	aag	gac	336
Ala	Gln	Glu	Trp	Cys	Arg	Lys	Tyr	Met	Lys	Ser	Gly	Asn	Val	Lys	Asp	
		100						105					110			
ctc	acg	caa	gcc	tgg	gac	ctc	tac	tat	cac	gtg	ttc	aga	cgg	atc	tca	384
Leu	Thr	Gln	Ala	Trp	Asp	Leu	Tyr	Tyr	His	Val	Phe	Arg	Arg	Ile	Ser	
		115					120					125				
aag	cag	cta	ccc	cag	ctc	aca	tcc	ctg	gag	ctg	cag	tat	gtg	tcc	ccc	432
Lys	Gln	Leu	Pro	Gln	Leu	Thr	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro	
	130					135					140					
aaa	ctt	ctg	atg	tgc	cga	gac	ctt	gag	ttg	gct	gtg	cca	gga	aca	tac	480
Lys	Leu	Leu	Met	Cys	Arg	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr	
145					150					155					160	
gac	ccc															486
Asp	Pro															

<210> 2
 <211> 162
 <212> PRT
 <213> Mouse

<400> 2																
Leu	Thr	Arg	His	Asn	Ala	Ala	Asn	Lys	Ile	Leu	Lys	Asn	Met	Cys	Glu	
1				5					10					15		
His	Ser	Asn	Thr	Leu	Val	Gln	Gln	Ala	Met	Met	Val	Ser	Glu	Glu	Leu	
		20						25				30				
Ile	Arg	Val	Ala	Ile	Leu	Trp	His	Glu	Met	Trp	His	Glu	Gly	Leu	Glu	
	35					40					45					
Glu	Ala	Ser	Arg	Leu	Tyr	Phe	Gly	Glu	Arg	Asn	Val	Lys	Gly	Met	Phe	
	50					55				60						
Glu	Val	Leu	Glu	Pro	Leu	His	Ala	Met	Met	Glu	Arg	Gly	Pro	Arg	Thr	
65				70					75					80		
Leu	Lys	Glu	Thr	Ser	Phe	Asn	Gln	Ala	Tyr	Gly	Arg	Asp	Leu	Met	Glu	
			85					90				95				
Ala	Gln	Glu	Trp	Cys	Arg	Lys	Tyr	Met	Lys	Ser	Gly	Asn	Val	Lys	Asp	
		100						105				110				
Leu	Thr	Gln	Ala	Trp	Asp	Leu	Tyr	Tyr	His	Val	Phe	Arg	Arg	Ile	Ser	
		115					120					125				
Lys	Gln	Leu	Pro	Gln	Leu	Thr	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro	
	130					135					140					
Lys	Leu	Leu	Met	Cys	Arg	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr	
145					150					155					160	
Asp	Pro															

<210> 3
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 3
 gggtttggaa ttcctaataa tgtctgtaca agtagaaacc 40

<210> 4
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 4
 gggtttcggg atcccgatcat tccagtttta gaac 34

<210> 5
 <211> 348
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14)...(325)

<400> 5
 ggaattccta ata atg tcc gta caa gta gaa acc atc tcc cca gga gac 49
 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp
 1 5 10

ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc 97
 Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
 15 20 25

ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc cgt gac cgt aac 145
 Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn
 30 35 40

aag ccc ttt aag ttt atg cta ggc aag cag gag gtg atc cga ggc tgg 193
 Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
 45 50 55 60

gaa gaa ggg gtt gcc cag atg agt gtg ggt cag cgt gcc aaa ctg act 241
 Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
 65 70 75

ata tct cca gat tat gcc tat ggt gcc act ggg cac cca ggc atc atc 289
 Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
 80 85 90

cca cca cat gcc act ctg gtc ttc gat gtg gag ctt ctaaaactgg 335
 Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
 95 100

aatgacggga tcc 348

<210> 6
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 6

```

Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
 1           5           10           15
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
      20           25           30
Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
      35           40           45
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
      50           55           60
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65           70           75           80
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
      85           90           95
Thr Leu Val Phe Asp Val Glu Leu
      100

```

<210> 7

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 7

tcgccggaat tcgggggcgagggtggagga gtacaagtag aaaccatc

48

<210> 8

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 8

gggttttcggg atcccgtcat tccagtttta gaag

34

<210> 9

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 9

cgcggatccg cgcattatta cttgttttga ttgatttttt g

41

<210> 10

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 10

cgcggatccg cgtaaaagca aagtactatc aattgagccg

40

<210> 11

<211> 5430

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(5427)

<400> 11

ttg	gag	cac	agt	ggg	att	gga	aga	atc	aaa	gag	cag	agt	gcc	cgc	atg	48
Leu	Glu	His	Ser	Gly	Ile	Gly	Arg	Ile	Lys	Glu	Gln	Ser	Ala	Arg	Met	
1				5					10					15		

ctg	ggg	cac	ctg	gtc	tcc	aat	gcc	ccc	cga	ctc	atc	cgc	ccc	tac	atg	96
Leu	Gly	His	Leu	Val	Ser	Asn	Ala	Pro	Arg	Leu	Ile	Arg	Pro	Tyr	Met	
			20					25					30			

gag	cct	att	ctg	aag	gca	tta	att	ttg	aaa	ctg	aaa	gat	cca	gac	cct	144
Glu	Pro	Ile	Leu	Lys	Ala	Leu	Ile	Leu	Lys	Leu	Lys	Asp	Pro	Asp	Pro	
		35					40					45				

gat	cca	aac	cca	ggg	gtg	atc	aat	aat	gtc	ctg	gca	aca	ata	gga	gaa	192
Asp	Pro	Asn	Pro	Gly	Val	Ile	Asn	Asn	Val	Leu	Ala	Thr	Ile	Gly	Glu	
	50					55					60					

ttg	gca	cag	gtt	agt	ggc	ctg	gaa	atg	agg	aaa	tgg	gtt	gat	gaa	ctt	240
Leu	Ala	Gln	Val	Ser	Gly	Leu	Glu	Met	Arg	Lys	Trp	Val	Asp	Glu	Leu	
65					70				75					80		

ttt	att	atc	atc	atg	gac	atg	ctc	cag	gat	tcc	tct	ttg	ttg	gcc	aaa	288
Phe	Ile	Ile	Ile	Met	Asp	Met	Leu	Gln	Asp	Ser	Ser	Leu	Leu	Ala	Lys	
				85					90					95		

agg	cag	gtg	gct	ctg	tgg	acc	ctg	gga	cag	ttg	gtg	gcc	agc	act	ggc	336
Arg	Gln	Val	Ala	Leu	Trp	Thr	Leu	Gly	Gln	Leu	Val	Ala	Ser	Thr	Gly	
			100					105					110			

tat	gta	gta	gag	ccc	tac	agg	aag	tac	cct	act	ttg	ctt	gag	gtg	cta	384
Tyr	Val	Val	Glu	Pro	Tyr	Arg	Lys	Tyr	Pro	Thr	Leu	Leu	Glu	Val	Leu	
			115				120						125			

ctg	aat	ttt	ctg	aag	act	gag	cag	aac	cag	ggg	aca	cgc	aga	gag	gcc	432
Leu	Asn	Phe	Leu	Lys	Thr	Glu	Gln	Asn	Gln	Gly	Thr	Arg	Arg	Glu	Ala	
	130					135					140					

atc	cgt	gtg	tta	ggg	ctt	tta	ggg	gct	ttg	gat	cct	tac	aag	cac	aaa	480
Ile	Arg	Val	Leu	Gly	Leu	Leu	Gly	Ala	Leu	Asp	Pro	Tyr	Lys	His	Lys	
145				150					155					160		

gtg	aac	att	ggc	atg	ata	gac	cag	tcc	cgg	gat	gcc	tct	gct	gtc	agc	528
Val	Asn	Ile	Gly	Met	Ile	Asp	Gln	Ser	Arg	Asp	Ala	Ser	Ala	Val	Ser	
			165					170					175			

ctg	tca	gaa	tcc	aag	tca	agt	cag	gat	tcc	tct	gac	tat	agc	act	agt	576
Leu	Ser	Glu	Ser	Lys	Ser	Ser	Gln	Asp	Ser	Ser	Asp	Tyr	Ser	Thr	Ser	
			180					185					190			

gaa atg ctg gtc aac atg gga aac ttg cct ctg gat gag ttc tac cca	624
Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu Phe Tyr Pro	
195 200 205	
gct gtg tcc atg gtg gcc ctg atg cgg atc ttc cga gac cag tca ctc	672
Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu	
210 215 220	
tct cat cat cac acc atg gtt gtc cag gcc atc acc ttc atc ttc aag	720
Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys	
225 230 235 240	
tcc ctg gga ctc aaa tgt gtg cag ttc ctg ccc cag gtc atg ccc acg	768
Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr	
245 250 255	
ttc ctt aat gtc att cga gtc tgt gat ggg gcc atc cgg gaa ttt ttg	816
Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile Arg Glu Phe Leu	
260 265 270	
ttc cag cag ctg gga atg ttg gtg tcc ttt gtg aag agc cac atc aga	864
Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys Ser His Ile Arg	
275 280 285	
cct tat atg gat gaa ata gtc acc ctc atg aga gaa ttc tgg gtc atg	912
Pro Tyr Met Asp Glu Ile Val Thr Leu Met Arg Glu Phe Trp Val Met	
290 295 300	
aac acc tca att cag agc acg atc att ctt ctc att gag caa att gtg	960
Asn Thr Ser Ile Gln Ser Thr Ile Ile Leu Leu Ile Glu Gln Ile Val	
305 310 315 320	
gta gct ctt ggg ggt gaa ttt aag ctc tac ctg ccc cag ctg atc cca	1008
Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro	
325 330 335	
cac atg ctg cgt gtc ttc atg cat gac aac agc cca ggc cgc att gtc	1056
His Met Leu Arg Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val	
340 345 350	
tct atc aag tta ctg gct gca atc cag ctg ttt ggc gcc aac ctg gat	1104
Ser Ile Lys Leu Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp	
355 360 365	
gac tac ctg cat tta ctg ctg cct cct att gtt aag ttg ttt gat gcc	1152
Asp Tyr Leu His Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala	
370 375 380	
cct gaa gct cca ctg cca tct cga aag gca gcg cta gag act gtg gac	1200
Pro Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp	
385 390 395 400	
cgc ctg acg gag tcc ctg gat ttc act gac tat gcc tcc cgg atc att	1248
Arg Leu Thr Glu Ser Leu Asp Phe Thr Asp Tyr Ala Ser Arg Ile Ile	
405 410 415	

cac cct att gtt cga aca ctg gac cag agc cca gaa ctg cgc tcc aca	1296
His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu Leu Arg Ser Thr	
420 425 430	
gcc atg gac acg ctg tct tca ctt gtt ttt cag ctg ggg aag aag tac	1344
Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu Gly Lys Lys Tyr	
435 440 445	
caa att ttc att cca atg gtg aat aaa gtt ctg gtg cga cac cga atc	1392
Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val Arg His Arg Ile	
450 455 460	
aat cat cag cgc tat gat gtg ctc atc tgc aga att gtc aag gga tac	1440
Asn His Gln Arg Tyr Asp Val Leu Ile Cys Arg Ile Val Lys Gly Tyr	
465 470 475 480	
aca ctt gct gat gaa gag gag gat cct ttg att tac cag cat cgg atg	1488
Thr Leu Ala Asp Glu Glu Glu Asp Pro Leu Ile Tyr Gln His Arg Met	
485 490 495	
ctt agg agt ggc caa ggg gat gca ttg gct agt gga cca gtg gaa aca	1536
Leu Arg Ser Gly Gln Gly Asp Ala Leu Ala Ser Gly Pro Val Glu Thr	
500 505 510	
gga ccc atg aag aaa ctg cac gtc agc acc atc aac ctc caa aag gcc	1584
Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn Leu Gln Lys Ala	
515 520 525	
tgg ggc gct gcc agg agg gtc tcc aaa gat gac tgg ctg gaa tgg ctg	1632
Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp Leu Glu Trp Leu	
530 535 540	
aga cgg ctg agc ctg gag ctg ctg aag gac tca tca tcg ccc tcc ctg	1680
Arg Arg Leu Ser Leu Glu Leu Leu Lys Asp Ser Ser Ser Pro Ser Leu	
545 550 555 560	
cgc tcc tgc tgg gcc ctg gca cag gcc tac aac ccg atg gcc agg gat	1728
Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro Met Ala Arg Asp	
565 570 575	
ctc ttc aat gct gca ttt gtg tcc tgc tgg tct gaa ctg aat gaa gat	1776
Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu Leu Asn Glu Asp	
580 585 590	
caa cag gat gag ctc atc aga agc atc gag ttg gcc ctc acc tca caa	1824
Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala Leu Thr Ser Gln	
595 600 605	
gac atc gct gaa gtc aca cag acc ctc tta aac ttg gct gaa ttc atg	1872
Asp Ile Ala Glu Val Thr Gln Thr Leu Leu Asn Leu Ala Glu Phe Met	
610 615 620	
gaa cac agt gac aag ggc ccc ctg cca ctg aga gat gac aat ggc att	1920
Glu His Ser Asp Lys Gly Pro Leu Pro Leu Arg Asp Asp Asn Gly Ile	
625 630 635 640	
gtt ctg ctg ggt gag aga gct gcc aag tgc cga gca tat gcc aaa gca	1968
Val Leu Leu Gly Glu Arg Ala Ala Lys Cys Arg Ala Tyr Ala Lys Ala	
645 650 655	

cta cac tac aaa gaa ctg gag ttc cag aaa ggc ccc acc cct gcc att	2016
Leu His Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro Thr Pro Ala Ile	
660 665 670	
cta gaa tct ctc atc agc att aat aat aag cta cag cag ccg gag gca	2064
Leu Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln Gln Pro Glu Ala	
675 680 685	
gcg gcc gga gtg tta gaa tat gcc atg aaa cac ttt gga gag ctg gag	2112
Ala Ala Gly Val Leu Glu Tyr Ala Met Lys His Phe Gly Glu Leu Glu	
690 695 700	
atc cag gct acc tgg tat gag aaa ctg cac gag tgg gag gat gcc ctt	2160
Ile Gln Ala Thr Trp Tyr Glu Lys Leu His Glu Trp Glu Asp Ala Leu	
705 710 715 720	
gtg gcc tat gac aag aaa atg gac acc aac aag gac gac cca gag ctg	2208
Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp Asp Pro Glu Leu	
725 730 735	
atg ctg ggc cgc atg cgc tgc ctc gag gcc ttg ggg gaa tgg ggt caa	2256
Met Leu Gly Arg Met Arg Cys Leu Glu Ala Leu Gly Glu Trp Gly Gln	
740 745 750	
ctc cac cag cag tgc tgt gaa aag tgg acc ctg gtt aat gat gag acc	2304
Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu Val Asn Asp Glu Thr	
755 760 765	
caa gcc aag atg gcc cgg atg gct gct gca gct gca tgg ggt tta ggt	2352
Gln Ala Lys Met Ala Arg Met Ala Ala Ala Ala Trp Gly Leu Gly	
770 775 780	
cag tgg gac agc atg gaa gaa tac acc tgt atg atc cct cgg gac acc	2400
Gln Trp Asp Ser Met Glu Glu Tyr Thr Cys Met Ile Pro Arg Asp Thr	
785 790 795 800	
cat gat ggg gca ttt tat aga gct gtg ctg gca ctg cat cag gac ctc	2448
His Asp Gly Ala Phe Tyr Arg Ala Val Leu Ala Leu His Gln Asp Leu	
805 810 815	
ttc tcc ttg gca caa cag tgc att gac aag gcc agg gac ctg ctg gat	2496
Phe Ser Leu Ala Gln Gln Cys Ile Asp Lys Ala Arg Asp Leu Leu Asp	
820 825 830	
gct gaa tta act gca atg gca gga gag agt tac agt cgg gca tat ggg	2544
Ala Glu Leu Thr Ala Met Ala Gly Glu Ser Tyr Ser Arg Ala Tyr Gly	
835 840 845	
gcc atg gtt tct tgc cac atg ctg tcc gag ctg gag gag gtt atc cag	2592
Ala Met Val Ser Cys His Met Leu Ser Glu Leu Glu Glu Val Ile Gln	
850 855 860	
tac aaa ctt gtc ccc gag cga cga gag atc atc cgc cag atc tgg tgg	2640
Tyr Lys Leu Val Pro Glu Arg Arg Glu Ile Ile Arg Gln Ile Trp Trp	
865 870 875 880	

9/24

gag aga ctg cag ggc tgc cag cgt atc gta gag gac tgg cag aaa atc	2688
Glu Arg Leu Gln Gly Cys Gln Arg Ile Val Glu Asp Trp Gln Lys Ile	
885 890 895	
ctt atg gtg cgg tcc ctt gtg gtc agc cct cat gaa gac atg aga acc	2736
Leu Met Val Arg Ser Leu Val Val Ser Pro His Glu Asp Met Arg Thr	
900 905 910	
tgg ctc aag tat gca agc ctg tgc ggc aag agt ggc agg ctg gct ctt	2784
Trp Leu Lys Tyr Ala Ser Leu Cys Gly Lys Ser Gly Arg Leu Ala Leu	
915 920 925	
gct cat aaa act tta gtg ttg ctc ctg gga gtt gat ccg tct cgg caa	2832
Ala His Lys Thr Leu Val Leu Leu Gly Val Asp Pro Ser Arg Gln	
930 935 940	
ctt gac cat cct ctg cca aca gtt cac cct cag gtg acc tat gcc tac	2880
Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val Thr Tyr Ala Tyr	
945 950 955 960	
atg aaa aac atg tgg aag agt gcc cgc aag atc gat gcc ttc cag cac	2928
Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp Ala Phe Gln His	
965 970 975	
atg cag cat ttt gtc cag acc atg cag caa cag gcc cag cat gcc atc	2976
Met Gln His Phe Val Gln Thr Met Gln Gln Gln Ala Gln His Ala Ile	
980 985 990	
gct act gag gac cag cag cat aag cag gaa ctg cac aag ctc atg gcc	3024
Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu His Lys Leu Met Ala	
995 1000 1005	
cga tgc ttc ctg aaa ctt gga gag tgg cag ctg aat cta cag ggc atc	3072
Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln Leu Asn Leu Gln Gly Ile	
1010 1015 1020	
aat gag agc aca atc ccc aaa gtg ctg cag tac tac agc gcc gcc aca	3120
Asn Glu Ser Thr Ile Pro Lys Val Leu Gln Tyr Tyr Ser Ala Ala Thr	
1025 1030 1035 1040	
gag cac gac cgc agc tgg tac aag gcc tgg cat gcg tgg gca gtg atg	3168
Glu His Asp Arg Ser Trp Tyr Lys Ala Trp His Ala Trp Ala Val Met	
1045 1050 1055	
aac ttc gaa gct gtg cta cac tac aaa cat cag aac caa gcc cgc gat	3216
Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn Gln Ala Arg Asp	
1060 1065 1070	
gag aag aag aaa ctg cgt cat gcc agc ggg gcc aac atc acc aac gcc	3264
Glu Lys Lys Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn Ala	
1075 1080 1085	
acc act gcc gcc acc acg gcc gcc act gcc acc acc act gcc agc acc	3312
Thr Thr Ala Ala Thr Thr Ala Ala Thr Ala Thr Thr Ala Ser Thr	
1090 1095 1100	
gag ggc agc aac agt gag agc gag gcc gag agc acc gag aac agc ccc	3360
Glu Gly Ser Asn Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser Pro	
1105 1110 1115 1120	

10/24

acc cca tgc ccg ctg cag aag aag gtc act gag gat ctg tcc aaa acc	3408
Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp Leu Ser Lys Thr	
1125 1130 1135	
ctc ctg atg tac acg gtg cct gcc gtc cag ggc ttc ttc cgt tcc atc	3456
Leu Leu Met Tyr Thr Val Pro Ala Val Gln Gly Phe Phe Arg Ser Ile	
1140 1145 1150	
tcc ttg tca cga ggc aac aac ctc cag gat aca ctc aga gtt ctc acc	3504
Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu Arg Val Leu Thr	
1155 1160 1165	
tta tgg ttt gat tat ggt cac tgg cca gat gtc aat gag gcc tta gtg	3552
Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn Glu Ala Leu Val	
1170 1175 1180	
gag ggg gtg aaa gcc atc cag att gat acc tgg cta cag gtt ata cct	3600
Glu Gly Val Lys Ala Ile Gln Ile Asp Thr Trp Leu Gln Val Ile Pro	
1185 1190 1195 1200	
cag ctc att gca aga att gat acg ccc aga ccc ttg gtg gga cgt ctc	3648
Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg Pro Leu Val Gly Arg Leu	
1205 1210 1215	
att cac cag ctt ctc aca gac att ggt cgg tac cac ccc cag gcc ctc	3696
Ile His Gln Leu Leu Thr Asp Ile Gly Arg Tyr His Pro Gln Ala Leu	
1220 1225 1230	
atc tac cca ctg aca gtg gct tct aag tct acc acg aca gcc cgg cac	3744
Ile Tyr Pro Leu Thr Val Ala Ser Lys Ser Thr Thr Thr Ala Arg His	
1235 1240 1245	
aat gca gcc aac aag att ctg aag aac atg tgt gag cac agc aac acc	3792
Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu His Ser Asn Thr	
1250 1255 1260	
ctg gtc cag cag gcc atg atg gtg agc gag gag ctg atc cga gtg gcc	3840
Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu Ile Arg Val Ala	
1265 1270 1275 1280	
atc ctc tgg cat gag atg tgg cat gaa ggc ctg gaa gag gca tct cgt	3888
Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg	
1285 1290 1295	
ttg tac ttt ggg gaa agg aac gtg aaa ggc atg ttt gag gtg ctg gag	3936
Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu	
1300 1305 1310	
ccc ttg cat gct atg atg gaa cgg ggc ccc cag act ctg aag gaa aca	3984
Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr	
1315 1320 1325	
tcc ttt aat cag gcc tat ggt cga gat tta atg gag gcc caa gag tgg	4032
Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp	
1330 1335 1340	

11/24

tgc agg aag tac atg aaa tca ggg aat gtc aag gac ctc acc caa gcc	4080
Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala	
1345 1350 1355 1360	
tgg gac ctc tat tat cat gtg ttc cga cga atc tca aag cag ctg cct	4128
Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu Pro	
1365 1370 1375	
cag ctc aca tcc tta gag ctg caa tat gtt tcc cca aaa ctt ctg atg	4176
Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu Met	
1380 1385 1390	
tgc cgg gac ctt gaa ttg gct gtg cca gga aca tat gac ccc aac cag	4224
Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn Gln	
1395 1400 1405	
cca atc att cgc att cag tcc ata gca ccg tct ttg caa gtc atc aca	4272
Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile Thr	
1410 1415 1420	
tcc aag cag agg ccc cgg aaa ttg aca ctt atg ggc agc aac gga cat	4320
Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly His	
1425 1430 1435 1440	
gag ttt gtt ttc ctt cta aaa ggc cat gaa gat ctg cgc cag gat gag	4368
Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp Glu	
1445 1450 1455	
cgt gtg atg cag ctc ttc ggc ctg gtt aac acc ctt ctg gcc aat gac	4416
Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Ala Asn Asp	
1460 1465 1470	
cca aca tct ctt cgg aaa aac ctc agc atc cag aga tac gct gtc atc	4464
Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg Tyr Ala Val Ile	
1475 1480 1485	
cct tta tcg acc aac tcg ggc ctc att ggc tgg gtt ccc cac tgt gac	4512
Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val Pro His Cys Asp	
1490 1495 1500	
aca ctg cac gcc ctc atc cgg gac tac agg gag aag aag aag atc ctt	4560
Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys Lys Lys Ile Leu	
1505 1510 1515 1520	
ctc aac atc gag cat cgc atc atg ttg cgg atg gct ccg gac tat gac	4608
Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala Pro Asp Tyr Asp	
1525 1530 1535	
cac ttg act ctg atg cag aag gtg gag gtg ttt gag cat gcc gtc aat	4656
His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu His Ala Val Asn	
1540 1545 1550	
aat aca gct ggg gac gac ctg gcc aag ctg ctg tgg ctg aaa agc ccc	4704
Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp Leu Lys Ser Pro	
1555 1560 1565	
agc tcc gag gtg tgg ttt gac cga aga acc aat tat acc cgt tct tta	4752
Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr Thr Arg Ser Leu	
1570 1575 1580	

gcg	gtc	atg	tca	atg	gtt	ggg	tat	att	tta	ggc	ctg	gga	gat	aga	cac	4800
Ala	Val	Met	Ser	Met	Val	Gly	Tyr	Ile	Leu	Gly	Leu	Gly	Asp	Arg	His	
1585					1590					1595					1600	
cca	tcc	aac	ctg	atg	ctg	gac	cgt	ctg	agt	ggg	aag	atc	ctg	cac	att	4848
Pro	Ser	Asn	Leu	Met	Leu	Asp	Arg	Leu	Ser	Gly	Lys	Ile	Leu	His	Ile	
				1605					1610					1615		
gac	ttt	ggg	gac	tgc	ttt	gag	gtt	gct	atg	acc	cga	gag	aag	ttt	cca	4896
Asp	Phe	Gly	Asp	Cys	Phe	Glu	Val	Ala	Met	Thr	Arg	Glu	Lys	Phe	Pro	
			1620					1625					1630			
gag	aag	att	cca	ttt	aga	cta	aca	aga	atg	ttg	acc	aat	gct	atg	gag	4944
Glu	Lys	Ile	Pro	Phe	Arg	Leu	Thr	Arg	Met	Leu	Thr	Asn	Ala	Met	Glu	
			1635				1640					1645				
gtt	aca	ggc	ctg	gat	ggc	aac	tac	aga	atc	aca	tgc	cac	aca	gtg	atg	4992
Val	Thr	Gly	Leu	Asp	Gly	Asn	Tyr	Arg	Ile	Thr	Cys	His	Thr	Val	Met	
	1650					1655					1660					
gag	gtg	ctg	cga	gag	cac	aag	gac	agt	gtc	atg	gcc	gtg	ctg	gaa	gcc	5040
Glu	Val	Leu	Arg	Glu	His	Lys	Asp	Ser	Val	Met	Ala	Val	Leu	Glu	Ala	
1665					1670				1675						1680	
ttt	gtc	tat	gac	ccc	ttg	ctg	aac	tgg	agg	ctg	atg	gac	aca	aat	acc	5088
Phe	Val	Tyr	Asp	Pro	Leu	Leu	Asn	Trp	Arg	Leu	Met	Asp	Thr	Asn	Thr	
				1685					1690					1695		
aaa	ggc	aac	aag	cga	tcc	cga	acg	agg	acg	gat	tcc	tac	tct	gct	ggc	5136
Lys	Gly	Asn	Lys	Arg	Ser	Arg	Thr	Arg	Thr	Asp	Ser	Tyr	Ser	Ala	Gly	
			1700					1705					1710			
cag	tca	gtc	gaa	att	ttg	gac	ggg	gtg	gaa	ctt	gga	gag	cca	gcc	cat	5184
Gln	Ser	Val	Glu	Ile	Leu	Asp	Gly	Val	Glu	Leu	Gly	Glu	Pro	Ala	His	
		1715					1720					1725				
aag	aaa	acg	ggg	acc	aca	gtg	cca	gaa	tct	att	cat	tct	ttc	att	gga	5232
Lys	Lys	Thr	Gly	Thr	Thr	Val	Pro	Glu	Ser	Ile	His	Ser	Phe	Ile	Gly	
	1730					1735					1740					
gac	ggg	ttg	gtg	aaa	cca	gag	gcc	cta	aat	aag	aaa	gct	atc	cag	att	5280
Asp	Gly	Leu	Val	Lys	Pro	Glu	Ala	Leu	Asn	Lys	Lys	Ala	Ile	Gln	Ile	
1745					1750					1755					1760	
att	aac	agg	gtt	cga	gat	aag	ctc	act	ggg	cgg	gac	ttc	tct	cat	gat	5328
Ile	Asn	Arg	Val	Arg	Asp	Lys	Leu	Thr	Gly	Arg	Asp	Phe	Ser	His	Asp	
				1765					1770					1775		
gac	act	ttg	gat	gtt	cca	acg	caa	gtt	gag	ctg	ctc	atc	aaa	caa	gcg	5376
Asp	Thr	Leu	Asp	Val	Pro	Thr	Gln	Val	Glu	Leu	Leu	Ile	Lys	Gln	Ala	
			1780					1785					1790			
aca	tcc	cat	gaa	aac												

<210> 12
 <211> 1809
 <212> PRT
 <213> Homo sapiens

<400> 12
 Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met
 1 5 10 15
 Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met
 20 25 30
 Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro
 35 40 45
 Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu
 50 55 60
 Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu
 65 70 75 80
 Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys
 85 90 95
 Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly
 100 105 110
 Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu
 115 120 125
 Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala
 130 135 140
 Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys
 145 150 155 160
 Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val Ser
 165 170 175
 Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp Tyr Ser Thr Ser
 180 185 190
 Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu Phe Tyr Pro
 195 200 205
 Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu
 210 215 220
 Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys
 225 230 235 240
 Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr
 245 250 255
 Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile Arg Glu Phe Leu
 260 265 270
 Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys Ser His Ile Arg
 275 280 285
 Pro Tyr Met Asp Glu Ile Val Thr Leu Met Arg Glu Phe Trp Val Met
 290 295 300
 Asn Thr Ser Ile Gln Ser Thr Ile Ile Leu Leu Ile Glu Gln Ile Val
 305 310 315 320
 Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro
 325 330 335
 His Met Leu Arg Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val
 340 345 350
 Ser Ile Lys Leu Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp
 355 360 365
 Asp Tyr Leu His Leu Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala
 370 375 380
 Pro Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp
 385 390 395 400

Arg	Leu	Thr	Glu	Ser	Leu	Asp	Phe	Thr	Asp	Tyr	Ala	Ser	Arg	Ile	Ile
				405					410					415	
His	Pro	Ile	Val	Arg	Thr	Leu	Asp	Gln	Ser	Pro	Glu	Leu	Arg	Ser	Thr
			420					425					430		
Ala	Met	Asp	Thr	Leu	Ser	Ser	Leu	Val	Phe	Gln	Leu	Gly	Lys	Lys	Tyr
		435					440					445			
Gln	Ile	Phe	Ile	Pro	Met	Val	Asn	Lys	Val	Leu	Val	Arg	His	Arg	Ile
	450					455					460				
Asn	His	Gln	Arg	Tyr	Asp	Val	Leu	Ile	Cys	Arg	Ile	Val	Lys	Gly	Tyr
465					470					475					480
Thr	Leu	Ala	Asp	Glu	Glu	Glu	Asp	Pro	Leu	Ile	Tyr	Gln	His	Arg	Met
				485				490						495	
Leu	Arg	Ser	Gly	Gln	Gly	Asp	Ala	Leu	Ala	Ser	Gly	Pro	Val	Glu	Thr
			500					505					510		
Gly	Pro	Met	Lys	Lys	Leu	His	Val	Ser	Thr	Ile	Asn	Leu	Gln	Lys	Ala
		515					520					525			
Trp	Gly	Ala	Ala	Arg	Arg	Val	Ser	Lys	Asp	Asp	Trp	Leu	Glu	Trp	Leu
	530					535					540				
Arg	Arg	Leu	Ser	Leu	Glu	Leu	Leu	Lys	Asp	Ser	Ser	Ser	Pro	Ser	Leu
545					550					555					560
Arg	Ser	Cys	Trp	Ala	Leu	Ala	Gln	Ala	Tyr	Asn	Pro	Met	Ala	Arg	Asp
				565					570					575	
Leu	Phe	Asn	Ala	Ala	Phe	Val	Ser	Cys	Trp	Ser	Glu	Leu	Asn	Glu	Asp
			580					585					590		
Gln	Gln	Asp	Glu	Leu	Ile	Arg	Ser	Ile	Glu	Leu	Ala	Leu	Thr	Ser	Gln
		595					600					605			
Asp	Ile	Ala	Glu	Val	Thr	Gln	Thr	Leu	Leu	Asn	Leu	Ala	Glu	Phe	Met
	610					615					620				
Glu	His	Ser	Asp	Lys	Gly	Pro	Leu	Pro	Leu	Arg	Asp	Asp	Asn	Gly	Ile
625					630					635					640
Val	Leu	Leu	Gly	Glu	Arg	Ala	Ala	Lys	Cys	Arg	Ala	Tyr	Ala	Lys	Ala
				645					650					655	
Leu	His	Tyr	Lys	Glu	Leu	Glu	Phe	Gln	Lys	Gly	Pro	Thr	Pro	Ala	Ile
			660					665					670		
Leu	Glu	Ser	Leu	Ile	Ser	Ile	Asn	Asn	Lys	Leu	Gln	Gln	Pro	Glu	Ala
		675					680					685			
Ala	Ala	Gly	Val	Leu	Glu	Tyr	Ala	Met	Lys	His	Phe	Gly	Glu	Leu	Glu
	690					695					700				
Ile	Gln	Ala	Thr	Trp	Tyr	Glu	Lys	Leu	His	Glu	Trp	Glu	Asp	Ala	Leu
705					710					715					720
Val	Ala	Tyr	Asp	Lys	Lys	Met	Asp	Thr	Asn	Lys	Asp	Asp	Pro	Glu	Leu
				725					730					735	
Met	Leu	Gly	Arg	Met	Arg	Cys	Leu	Glu	Ala	Leu	Gly	Glu	Trp	Gly	Gln
			740				745						750		
Leu	His	Gln	Gln	Cys	Cys	Glu	Lys	Trp	Thr	Leu	Val	Asn	Asp	Glu	Thr
		755					760					765			
Gln	Ala	Lys	Met	Ala	Arg	Met	Ala	Ala	Ala	Ala	Ala	Trp	Gly	Leu	Gly
	770					775					780				
Gln	Trp	Asp	Ser	Met	Glu	Glu	Tyr	Thr	Cys	Met	Ile	Pro	Arg	Asp	Thr
785					790					795					800
His	Asp	Gly	Ala	Phe	Tyr	Arg	Ala	Val	Leu	Ala	Leu	His	Gln	Asp	Leu
				805					810					815	
Phe	Ser	Leu	Ala	Gln	Gln	Cys	Ile	Asp	Lys	Ala	Arg	Asp	Leu	Leu	Asp
			820					825					830		
Ala	Glu	Leu	Thr	Ala	Met	Ala	Gly	Glu	Ser	Tyr	Ser	Arg	Ala	Tyr	Gly
		835					840					845			
Ala	Met	Val	Ser	Cys	His	Met	Leu	Ser	Glu	Leu	Glu	Glu	Val	Ile	Gln
	850					855					860				

Tyr	Lys	Leu	Val	Pro	Glu	Arg	Arg	Glu	Ile	Ile	Arg	Gln	Ile	Trp	Trp	865	870	875	880
Glu	Arg	Leu	Gln	Gly	Cys	Gln	Arg	Ile	Val	Glu	Asp	Trp	Gln	Lys	Ile				
				885					890						895				
Leu	Met	Val	Arg	Ser	Leu	Val	Val	Ser	Pro	His	Glu	Asp	Met	Arg	Thr				
			900					905					910						
Trp	Leu	Lys	Tyr	Ala	Ser	Leu	Cys	Gly	Lys	Ser	Gly	Arg	Leu	Ala	Leu				
		915					920					925							
Ala	His	Lys	Thr	Leu	Val	Leu	Leu	Leu	Gly	Val	Asp	Pro	Ser	Arg	Gln				
		930				935					940								
Leu	Asp	His	Pro	Leu	Pro	Thr	Val	His	Pro	Gln	Val	Thr	Tyr	Ala	Tyr				
945					950					955					960				
Met	Lys	Asn	Met	Trp	Lys	Ser	Ala	Arg	Lys	Ile	Asp	Ala	Phe	Gln	His				
				965					970						975				
Met	Gln	His	Phe	Val	Gln	Thr	Met	Gln	Gln	Gln	Ala	Gln	His	Ala	Ile				
			980					985					990						
Ala	Thr	Glu	Asp	Gln	Gln	His	Lys	Gln	Glu	Leu	His	Lys	Leu	Met	Ala				
		995					1000					1005							
Arg	Cys	Phe	Leu	Lys	Leu	Gly	Glu	Trp	Gln	Leu	Asn	Leu	Gln	Gly	Ile				
	1010				1015					1020									
Asn	Glu	Ser	Thr	Ile	Pro	Lys	Val	Leu	Gln	Tyr	Tyr	Ser	Ala	Ala	Thr				
1025				1030						1035					1040				
Glu	His	Asp	Arg	Ser	Trp	Tyr	Lys	Ala	Trp	His	Ala	Trp	Ala	Val	Met				
				1045					1050						1055				
Asn	Phe	Glu	Ala	Val	Leu	His	Tyr	Lys	His	Gln	Asn	Gln	Ala	Arg	Asp				
			1060					1065					1070						
Glu	Lys	Lys	Lys	Leu	Arg	His	Ala	Ser	Gly	Ala	Asn	Ile	Thr	Asn	Ala				
		1075					1080					1085							
Thr	Thr	Ala	Ala	Thr	Thr	Ala	Ala	Thr	Ala	Thr	Thr	Thr	Ala	Ser	Thr				
	1090					1095					1100								
Glu	Gly	Ser	Asn	Ser	Glu	Ser	Glu	Ala	Glu	Ser	Thr	Glu	Asn	Ser	Pro				
1105				1110						1115					1120				
Thr	Pro	Ser	Pro	Leu	Gln	Lys	Lys	Val	Thr	Glu	Asp	Leu	Ser	Lys	Thr				
				1125					1130						1135				
Leu	Leu	Met	Tyr	Thr	Val	Pro	Ala	Val	Gln	Gly	Phe	Phe	Arg	Ser	Ile				
			1140					1145					1150						
Ser	Leu	Ser	Arg	Gly	Asn	Asn	Leu	Gln	Asp	Thr	Leu	Arg	Val	Leu	Thr				
	1155						1160					1165							
Leu	Trp	Phe	Asp	Tyr	Gly	His	Trp	Pro	Asp	Val	Asn	Glu	Ala	Leu	Val				
	1170					1175					1180								
Glu	Gly	Val	Lys	Ala	Ile	Gln	Ile	Asp	Thr	Trp	Leu	Gln	Val	Ile	Pro				
1185					1190					1195					1200				
Gln	Leu	Ile	Ala	Arg	Ile	Asp	Thr	Pro	Arg	Pro	Leu	Val	Gly	Arg	Leu				
				1205					1210						1215				
Ile	His	Gln	Leu	Leu	Thr	Asp	Ile	Gly	Arg	Tyr	His	Pro	Gln	Ala	Leu				
			1220					1225					1230						
Ile	Tyr	Pro	Leu	Thr	Val	Ala	Ser	Lys	Ser	Thr	Thr	Thr	Ala	Arg	His				
	1235						1240					1245							
Asn	Ala	Ala	Asn	Lys	Ile	Leu	Lys	Asn	Met	Cys	Glu	His	Ser	Asn	Thr				
	1250					1255					1260								
Leu	Val	Gln	Gln	Ala	Met	Met	Val	Ser	Glu	Glu	Leu	Ile	Arg	Val	Ala				
1265					1270					1275					1280				
Ile	Leu	Trp	His	Glu	Met	Trp	His	Glu	Gly	Leu	Glu	Glu	Ala	Ser	Arg				
				1285					1290						1295				
Leu	Tyr	Phe	Gly	Glu	Arg	Asn	Val	Lys	Gly	Met	Phe	Glu	Val	Leu	Glu				
			1300					1305					1310						
Pro	Leu	His	Ala	Met	Met	Glu	Arg	Gly	Pro	Gln	Thr	Leu	Lys	Glu	Thr				
	1315						1320						1325						

Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp
 1330 1335 1340
 Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala
 1345 1350 1355 1360
 Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu Pro
 1365 1370 1375
 Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu Met
 1380 1385 1390
 Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn Gln
 1395 1400 1405
 Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile Thr
 1410 1415 1420
 Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly His
 1425 1430 1435 1440
 Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp Glu
 1445 1450 1455
 Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Ala Asn Asp
 1460 1465 1470
 Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg Tyr Ala Val Ile
 1475 1480 1485
 Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val Pro His Cys Asp
 1490 1495 1500
 Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys Lys Lys Ile Leu
 1505 1510 1515 1520
 Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala Pro Asp Tyr Asp
 1525 1530 1535
 His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu His Ala Val Asn
 1540 1545 1550
 Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp Leu Lys Ser Pro
 1555 1560 1565
 Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr Thr Arg Ser Leu
 1570 1575 1580
 Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His
 1585 1590 1595 1600
 Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys Ile Leu His Ile
 1605 1610 1615
 Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg Glu Lys Phe Pro
 1620 1625 1630
 Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr Asn Ala Met Glu
 1635 1640 1645
 Val Thr Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys His Thr Val Met
 1650 1655 1660
 Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu Glu Ala
 1665 1670 1675 1680
 Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp Thr Asn Thr
 1685 1690 1695
 Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser Tyr Ser Ala Gly
 1700 1705 1710
 Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly Glu Pro Ala His
 1715 1720 1725
 Lys Lys Thr Gly Thr Thr Val Pro Glu Ser Ile His Ser Phe Ile Gly
 1730 1735 1740
 Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys Ala Ile Gln Ile
 1745 1750 1755 1760
 Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp Phe Ser His Asp
 1765 1770 1775
 Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Leu Ile Lys Gln Ala
 1780 1785 1790

Thr Ser His Glu Asn Leu Cys Gln Cys Tyr Ile Gly Trp Cys Pro Phe
 1795 1800 1805
 Trp

<210> 13
 <211> 1794
 <212> DNA
 <213> C. albicans

<400> 13
 ttggtttacc ctttgacagt tgctattact tccgaatcaa cgagccgtaa aaaggcagct 60
 caatccatta ttgaaaaaat gcgagtacat tctcctagct tgggtggatca agcagaatta 120
 gtgagtcgag aactcatccg agttgcagtt ttatggcacg aacaatggca cgatgctttg 180
 gaagatgcta gcagggtttt ctttggtgaa cacaacacag aaaagatgtt tgaaacattg 240
 gaaccattac atcaaagtgt gcaaaagggg ccagaaacga tgagggaaca agcctttgca 300
 aatgcttttg gcagggagtt gacagatgca tacgagtggg tgctcaactt tagaagaact 360
 aaagacataa ccaatttgaa tcaagcatgg gatataact acaatgtctt tagaagagta 420
 agcaaacagg tgcagctggt agctagtctt gagttgcagt atgtatctcc ggacttagag 480
 catgctcaag atttggaatt ggctgtacca ggtacttacc aagcaggcaa acctgtgatc 540
 agaataatca aatttgatcc tactttttcg attatttcat ctaaacaag accgagaaaa 600
 ttatcgtgca gaggaagtga tggtaaagac taccaatatg cgttgaaagg acatgaagat 660
 atcagacaag ataacttagt gatgcaattg tttggtttgg ttaatacgtt gttggtaaat 720
 gatccggtat gtttcaagag acatttggat atacaacaat atcctgctat tccattatca 780
 ccaaaagtgg gattgcttgg ttgggttcca aatagtgaca ctttccatgt attgatcaaa 840
 ggctatcgcg aatcaagaag tataatgttg aatattgaac acaggctttt gttgcaaagt 900
 gcacctgatt atgatttctt gacattattg caaaaagttg aagtgttcac aagtgcaatg 960
 gataattgta agggacagga tttgtacaaa gtgttatggc tcaaactctaa atcatccgag 1020
 gcgtggttgg accgtagaac aacatacacg agatcattag ctgtaatgtc tatggttggg 1080
 tatatatagg gtttggggga taggcaccca tcaaatttga tgttggaccg tattactggg 1140
 aaagtcattcc atattgattt cggagactgt tttgaagcag caatattacg tgagaagtat 1200
 ccagagagag ttccgtttag attgacgaga atgcttaatt atgccatgga agttagtgga 1260
 atagagggct cgttcagaat cacatgtgaa catgttatga ggggtgttgcg tgataataaa 1320
 gagtctttta tggcaatatt agaggccttt gcttacgatc ccttgataaa ttggggggtt 1380
 gatttcccaa caaaggcggt ggctgaatca acgggtatac gtgttccaca agtcaacact 1440
 gcagaattat tacgcagagg acagattgac gaaaaagaag ctgtaagatt gcaaaagcaa 1500
 aatgaattgg aaataagaaa cgctagagct gcattagtgt tgaaacgtat taccgataag 1560
 ttaactggta acgatatcaa acggttgaga ggattagatg tgcctactca agtcgataaa 1620
 ttgattcaac aagccaccag tgttgagaat ttgtgtcagc attacattgg ttggtgttcg 1680
 tgttggtagg ttgattatcg tcatgtgtcg ataagtatgg tattgtggta actattttat 1740
 aaagggaaat attaaagaat tgtatattat taaaaaaaaa aaaaaaaact cgag 1794

<210> 14
 <211> 562
 <212> PRT
 <213> C. albicans

<400> 14
 Leu Val Tyr Pro Leu Thr Val Ala Ile Thr Ser Glu Ser Thr Ser Arg
 1 5 10 15
 Lys Lys Ala Ala Gln Ser Ile Ile Glu Lys Met Arg Val His Ser Pro
 20 25 30
 Ser Leu Val Asp Gln Ala Glu Leu Val Ser Arg Glu Leu Ile Arg Val
 35 40 45
 Ala Val Leu Trp His Glu Gln Trp His Asp Ala Leu Glu Asp Ala Ser
 50 55 60
 Arg Phe Phe Phe Gly Glu His Asn Thr Glu Lys Met Phe Glu Thr Leu
 65 70 75 80

Glu	Pro	Leu	His	Gln	Met	Leu	Gln	Lys	Gly	Pro	Glu	Thr	Met	Arg	Glu
			85						90					95	
Gln	Ala	Phe	Ala	Asn	Ala	Phe	Gly	Arg	Glu	Leu	Thr	Asp	Ala	Tyr	Glu
		100					105						110		
Trp	Val	Leu	Asn	Phe	Arg	Arg	Thr	Lys	Asp	Ile	Thr	Asn	Leu	Asn	Gln
	115						120					125			
Ala	Trp	Asp	Ile	Tyr	Tyr	Asn	Val	Phe	Arg	Arg	Val	Ser	Lys	Gln	Val
	130					135					140				
Gln	Leu	Leu	Ala	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro	Asp	Leu	Glu
145					150					155					160
His	Ala	Gln	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr	Gln	Ala	Gly
			165						170					175	
Lys	Pro	Val	Ile	Arg	Ile	Ile	Lys	Phe	Asp	Pro	Thr	Phe	Ser	Ile	Ile
		180						185					190		
Ser	Ser	Lys	Gln	Arg	Pro	Arg	Lys	Leu	Ser	Cys	Arg	Gly	Ser	Asp	Gly
	195						200					205			
Lys	Asp	Tyr	Gln	Tyr	Ala	Leu	Lys	Gly	His	Glu	Asp	Ile	Arg	Gln	Asp
	210					215					220				
Asn	Leu	Val	Met	Gln	Leu	Phe	Gly	Leu	Val	Asn	Thr	Leu	Leu	Val	Asn
225					230					235					240
Asp	Pro	Val	Cys	Phe	Lys	Arg	His	Leu	Asp	Ile	Gln	Gln	Tyr	Pro	Ala
			245						250					255	
Ile	Pro	Leu	Ser	Pro	Lys	Val	Gly	Leu	Leu	Gly	Trp	Val	Pro	Asn	Ser
		260					265						270		
Asp	Thr	Phe	His	Val	Leu	Ile	Lys	Gly	Tyr	Arg	Glu	Ser	Arg	Ser	Ile
	275						280					285			
Met	Leu	Asn	Ile	Glu	His	Arg	Leu	Leu	Leu	Gln	Met	Ala	Pro	Asp	Tyr
	290					295					300				
Asp	Phe	Leu	Thr	Leu	Leu	Gln	Lys	Val	Glu	Val	Phe	Thr	Ser	Ala	Met
305					310					315					320
Asp	Asn	Cys	Lys	Gly	Gln	Asp	Leu	Tyr	Lys	Val	Leu	Trp	Leu	Lys	Ser
			325						330					335	
Lys	Ser	Ser	Glu	Ala	Trp	Leu	Asp	Arg	Arg	Thr	Thr	Tyr	Thr	Arg	Ser
		340					345						350		
Leu	Ala	Val	Met	Ser	Met	Val	Gly	Tyr	Ile	Leu	Gly	Leu	Gly	Asp	Arg
	355						360					365			
His	Pro	Ser	Asn	Leu	Met	Leu	Asp	Arg	Ile	Thr	Gly	Lys	Val	Ile	His
	370					375					380				
Ile	Asp	Phe	Gly	Asp	Cys	Phe	Glu	Ala	Ala	Ile	Leu	Arg	Glu	Lys	Tyr
385					390					395					400
Pro	Glu	Arg	Val	Pro	Phe	Arg	Leu	Thr	Arg	Met	Leu	Asn	Tyr	Ala	Met
			405						410					415	
Glu	Val	Ser	Gly	Ile	Glu	Gly	Ser	Phe	Arg	Ile	Thr	Cys	Glu	His	Val
		420						425					430		
Met	Arg	Val	Leu	Arg	Asp	Asn	Lys	Glu	Ser	Leu	Met	Ala	Ile	Leu	Glu
	435						440					445			
Ala	Phe	Ala	Tyr	Asp	Pro	Leu	Ile	Asn	Trp	Gly	Phe	Asp	Phe	Pro	Thr
	450					455					460				
Lys	Ala	Leu	Ala	Glu	Ser	Thr	Gly	Ile	Arg	Val	Pro	Gln	Val	Asn	Thr
465					470					475					480
Ala	Glu	Leu	Leu	Arg	Arg	Gly	Gln	Ile	Asp	Glu	Lys	Glu	Ala	Val	Arg
			485						490					495	
Leu	Gln	Lys	Gln	Asn	Glu	Leu	Glu	Ile	Arg	Asn	Ala	Arg	Ala	Ala	Leu
		500						505					510		
Val	Leu	Lys	Arg	Ile	Thr	Asp	Lys	Leu	Thr	Gly	Asn	Asp	Ile	Lys	Arg
	515						520					525			
Leu	Arg	Gly	Leu	Asp	Val	Pro	Thr	Gln	Val	Asp	Lys	Leu	Ile	Gln	Gln
	530					535					540				

19/24

Ala Thr Ser Val Glu Asn Leu Cys Gln His Tyr Ile Gly Trp Cys Ser
545 550 555 560
Cys Trp

<210> 15
<211> 399
<212> DNA
<213> Homo sapiens

<400> 15
gtttagtcacg agttgatcag agtagccggt ctatggcacg aattatggta tgaaggactg 60
gaagatgcga gccgccaatt tttcgttgaa cataacatag aaaaaatggt ttctacttta 120
gaacctttac ataaacactt aggcaatgag cctcaaactg taagtgaggt atcgtttcag 180
aaatcatttg gtagagattt gaacgatgcc tacgaatggt tgaataacta caaaaagtca 240
aaagacatca ataatttgaa ccaagcttgg gatattttatt ataacgtctt cagaaaaata 300
acacgtcaaa taccacagtt acaaacctta gacttacagc atgtttctcc ccagcttctg 360
gctactcatg atctcgaatt ggctgttcct gggacatat 399

<210> 16
<211> 133
<212> PRT
<213> Homo sapiens

<400> 16
Val Ser His Glu Leu Ile Arg Val Ala Val Leu Trp His Glu Leu Trp
1 5 10 15
Tyr Glu Gly Leu Glu Asp Ala Ser Arg Gln Phe Phe Val Glu His Asn
20 25 30
Ile Glu Lys Met Phe Ser Thr Leu Glu Pro Leu His Lys His Leu Gly
35 40 45
Asn Glu Pro Gln Thr Leu Ser Glu Val Ser Phe Gln Lys Ser Phe Gly
50 55 60
Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Asn Asn Tyr Lys Lys Ser
65 70 75 80
Lys Asp Ile Asn Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
85 90 95
Phe Arg Lys Ile Thr Arg Gln Ile Pro Gln Leu Gln Thr Leu Asp Leu
100 105 110
Gln His Val Ser Pro Gln Leu Leu Ala Thr His Asp Leu Glu Leu Ala
115 120 125
Val Pro Gly Thr Tyr
130

<210> 17
<211> 399
<212> DNA
<213> Homo sapiens

<400> 17
gtcagccacg aattgatacg tatggcggtg ctttggcatg agcaatggta tgagggtctg 60
gatgacgccg gtaggcagtt ttttgagaga cataataccg aaaaaatggt tgctgcttta 120
gagcctctgt acgaaatgct gaagagagga ccggaaactt tgagggaaat atcgttccaa 180
aattcttttg gtagggactt gaatgacgct tacgaatggc tgatgaatta caaaaaatct 240
aaagatgtta gtaatttaaa ccaagcgtgg gacatttact ataatgtttt caggaaaatt 300
ggtaaacagt tgccacaatt acaaactctt gaactacaac atgtgtcgcc aaaactacta 360
tctgcgcgat atttggaatt ggctgtcccc gggaccgt 399

<210> 18
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 18
 Val Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp
 1 5 10 15
 Tyr Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn
 20 25 30
 Thr Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys
 35 40 45
 Arg Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly
 50 55 60
 Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser
 65 70 75 80
 Lys Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
 85 90 95
 Phe Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu
 100 105 110
 Gln His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala
 115 120 125
 Val Pro Gly Thr Arg
 130

<210> 19
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 59, 64, 72, 74, 89, 94, 101, 137, 158, 175, 190, 201, 207,
 210, 213, 218, 234, 243, 257, 283, 286, 289, 292, 314, 325,
 328, 335, 352, 361, 380, 384, 390, 393, 403, 411, 413, 427,
 432, 435, 440, 443, 450, 452, 460, 465, 480, 482, 486
 <223> n = A,T,C or G

<221> misc_feature
 <222> 492, 515
 <223> n = A,T,C or G

<400> 19
 tgaccctcac cccttccacc tatcccaaaa acctcactgg gtctgtggac aaacaacana 60
 aatnttttcc ananaggccc caaatgagnc ccanggggtct ntcttccatc agaccctagt 120
 attctgcgac tcacacnctt caattcaaga cctgaccnct agtagggagg ttantcaga 180
 tcgctggcan cctcggtga ncagatncan agnggggntc gctgttcagt gggncacccc 240
 tcnctggcct tcttcancag ggggtctggga tgttttcagt ggncnaana cnctgtttag 300
 agccagggct cagnaaacag aaaanctntc atggngggttc tggacacagg gnagggtctgg 360
 nacatattgg ggattatgan cagnaccaan acnccactaa atnccccaag nanaaagtgt 420
 aacctntct anacnccatn ttntatcagn anaaattttt ttccnataaa tgacatcagn 480
 antttnaaca tnaaaaaaaaa aaaaaaaaaa aaaaanaaaaa aaaaaaaaaa a 531

<210> 20
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 20
gcgtataacg cgtttgggaat cactacaggg atgtttaata ccactacaat ggatgatgta 60
tataactatc tattcgatga tgaagatacc ccaccaaacc caaaaaaaga gatctggaat 120
tcggatcctc gagagatcta tgaatcgtag atactgaaaa accccgcaag ttcacttcaa 180
ctgtgcatcg tgcaccatct caatttcttt catttataca tcgttttgcc t 231

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 21
tgaagatacc ccaccaaacc c 21

<210> 22
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 22
tgcacagttg aagtgaac 18

<210> 23
<211> 662
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 27, 373, 443, 461, 483, 485, 507, 583, 588, 593, 605, 606,
607, 612, 624, 625, 626, 627, 628, 630, 631, 632, 635, 639,
646, 652, 659, 661
<223> n = A,T,C or G

<400> 23
accaaaccga aaaaaagaga tcctagnaac tagtggatcc cccgggctgc aggaattcgg 60
tacgagtcgc cctcagcaga ctgcgccagg agaggaaagc atggaggaaa gaccacccat 120
ttggtttcgt ggctgtccca acaaaaaatc ccgatggcac gatgaacctc atgaactggg 180
agtgcgccat tccaggaaag aaagggactc cgtgggaagg aggcttggtt aaactacgga 240
tgcttttcaa agatgattat ccattcttcgc caccaaaatg taaattcgaa ccaccattat 300
ttcacccgaa tgtgtaccct tcggggacag tgtgcctgtc catcttagag gaggacaagg 360
actggagggc agncatcaca atcaaacagg atcctattag gaatacagga actttctaaa 420
tgaaccaa atccaagacc agntcaagca gagggctaca ngatttactg ccaaaacaga 480
gtngngtacg agaaagggtc cgagcanagc cagaagtttg ggcctcatta gcaggacact 540
gggtggatcgt caaaggaggt ttggttgagg agacttggtc aanatttngg aanttaagtt 600
gtccnnaaac tngcgggggg gggnnnnncn nnttnccant tccctncccc cngtthttng 660
nt 662

<210> 24
<211> 119
<212> PRT
<213> Homo sapiens

<220>

<221> VARIANT

<222> 105

<223> Xaa = Any Amino Acid

<400> 24

```

Val Arg Val Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg
 1           5           10           15
Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro Asp
           20           25           30
Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys
           35           40           45
Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe Lys
           50           55           60
Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu
65           70           75           80
Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu
           85           90           95
Glu Glu Asp Lys Asp Trp Arg Ala Xaa Ile Thr Ile Lys Gln Asp Pro
           100          105          110
Ile Arg Asn Thr Gly Thr Phe
           115

```

<210> 25

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<221> misc_feature

<222> 112, 148, 158, 171, 178, 182, 191, 194, 203, 204

<223> n = A,T,C or G

<400> 25

```

ccctccctcc tgccgctcct ctctagaacc ttctagaacc tgggctgtgc tgcttttgag 60
cctcagaccc cagggcagca tctcggttct gcgccacttc ctttgtgttt anatggcggt 120
ttgtctgtgt tgctgtttag agtagatnaa ctgtttanat aaaaaaaaaa naaaattnac 180
tngagggggc ntgnaggcat gcnaac 207

```

<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 26

gaagaggcaa gacgcttgta c

21

<210> 27

<211> 21

<212> DNA

<213> Homo sapiens

<400> 27

gtacaagcgt cttgcctctt c 21

<210> 28
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 28
 gagtttgagc agatgttta 19

<210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> misc_feature
 <222> 3, 9, 15
 <223> n = A,T,C or G

<400> 29
 ggnaargcnc ayccncargc 20

<210> 30
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> misc_feature
 <222> 3, 6, 21
 <223> n = A,T,C or G

<400> 30
 atngcnggrt aytgytgdat ntc 23

<210> 31
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 31
 grgayttraw bgabgchyam gawtgg 26

<210> 32
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 32

caagcbtggg aymtymtyta ytatmaygtb ttcag

35

<210> 33

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 33

gayybgartt ggctgtbcch gg

22

<210> 34

<211> 327

<212> DNA

<213> Homo sapiens

<400> 34

atgtccgtac	aagtagaaac	catctcccca	ggagacgggc	gcaccttccc	caagcgcggc	60
cagacctgcg	tggtgcacta	caccgggatg	cttgaagatg	gaaagaaatt	tgattcctcc	120
cgtgaccgta	acaagccctt	taagtttatg	ctaggcaagc	aggaggtgat	ccgaggctgg	180
gaagaagggg	ttgccagat	gagtgtgggt	cagcgtgcca	aactgactat	atctccagat	240
tatgcctatg	gtgccactgg	gcaccaggc	atcatccac	cacatgccac	tctcgtcttc	300
gatgtggagc	ttctaaaact	ggaatga				327

<210> 35

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 35

gagatctgga attcggatcc tcgagagatc t

31